



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Yu, Guo-Liang
Rosen, Craig
- (ii) TITLE OF INVENTION: Colon Specific Genes and Proteins
- (iii) NUMBER OF SEQUENCES: 24
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
Stewart & Olstein
 - (B) STREET: 6 Becker Farm Road
 - (C) CITY: Roseland
 - (D) STATE: NJ
 - (E) COUNTRY: USA
 - (F) ZIP: 07068-1739
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/469,667
 - (B) FILING DATE: 06-JUN-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ferraro, Gregory D.
 - (B) REGISTRATION NUMBER: 36,134
 - (C) REFERENCE/DOCKET NUMBER: 325800-435
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-994-1700
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 638 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..501

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCC AGG CAG CTG GCT GCC SAC CAG GCC GTG TAT GTG AAG GTC AAG GCT	48
Ala Arg Gln Leu Ala Ala Xaa Gln Ala Val Tyr Val Lys Val Lys Ala	
1 5 10 15	
GAA GCC CGG GAA CTG CTG GGC CAC CCG TGG TCT CTG TGT CCT GTC TGT	96
Glu Ala Arg Glu Leu Leu Gly His Pro Trp Ser Leu Cys Pro Val Cys	
20 25 30	
GGG TGC CAA CTC ACC ACC TTT GAT GGG GCC CGT GGT GCC ACC ACT CTC	144
Gly Cys Gln Leu Thr Thr Phe Asp Gly Ala Arg Gly Ala Thr Thr Leu	
35 40 45	
CTG GTG TCT ATG AAG CTC TCT TCC CGC TGC CCA GGA CTA CAG AAT ACC	192
Leu Val Ser Met Lys Leu Ser Ser Arg Cys Pro Gly Leu Gln Asn Thr	
50 55 60	
ATC CCC TGG TAC CGT GTA GTT GCC GAA GTC CAG ATC TGC CAT GGC AAA	240
Ile Pro Trp Tyr Arg Val Val Ala Glu Val Gln Ile Cys His Gly Lys	
65 70 75 80	
ACG GAG GCT GTG GGC CAG GTC CAC ATC TTC TTC CAG GAT GGG ATG GTG	288
Thr Glu Ala Val Gly Gln Val His Ile Phe Phe Gln Asp Gly Met Val	
85 90 95	
ACG TTG ACT CCA AAC AAG GGT GTG TGG GTG AAT GGT CTC CGA GTG GAT	336
Thr Leu Thr Pro Asn Lys Gly Val Trp Val Asn Gly Leu Arg Val Asp	
100 105 110	
CTC CCA GCT GAG AAG TTA GCA TCT GTG TCC GTG AGT CGT ACA CCT GAT	384
Leu Pro Ala Glu Lys Leu Ala Ser Val Ser Val Ser Arg Thr Pro Asp	
115 120 125	
GGC TCC CTG CTA GTC CGC CAG AAG GCA GGG GTC CAG GTG TGG CTT GGA	432
Gly Ser Leu Leu Val Arg Gln Lys Ala Gly Val Gln Val Trp Leu Gly	
130 135 140	
GCC AAT GGG AAG GTG GCT GTG ATT GTG AGC AAT GAC CAT GCT GGG AAA	480
Ala Asn Gly Lys Val Ala Val Ile Val Ser Asn Asp His Ala Gly Lys	
145 150 155 160	
CTG TGT GGG GGC CTK TGG AAA ATTTGACGGG GGACCAGACC AATGATTGGG	531
Leu Cys Gly Gly Xaa Trp Lys	
165	
ATGATTCCCA GGAGAAGCCA GCGATTGGGG AAWTGGAGAG CGCAGGGACT TTCTYCCMCA	591
TGTTAATGGG CTTGWTCCAG TTCATCCCAC CAGGAACGAA GGATTTT	638

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Arg Gln Leu Ala Ala Xaa Gln Ala Val Tyr Val Lys Val Lys Ala
1 5 10 15
Glu Ala Arg Glu Leu Leu Gly His Pro Trp Ser Leu Cys Pro Val Cys
20 25 30
Gly Cys Gln Leu Thr Thr Phe Asp Gly Ala Arg Gly Ala Thr Thr Leu
35 40 45
Leu Val Ser Met Lys Leu Ser Ser Arg Cys Pro Gly Leu Gln Asn Thr
50 55 60
Ile Pro Trp Tyr Arg Val Val Ala Glu Val Gln Ile Cys His Gly Lys
65 70 75 80
Thr Glu Ala Val Gly Gln Val His Ile Phe Phe Gln Asp Gly Met Val
85 90 95
Thr Leu Thr Pro Asn Lys Gly Val Trp Val Asn Gly Leu Arg Val Asp
100 105 110
Leu Pro Ala Glu Lys Leu Ala Ser Val Ser Val Ser Arg Thr Pro Asp
115 120 125
Gly Ser Leu Leu Val Arg Gln Lys Ala Gly Val Gln Val Trp Leu Gly
130 135 140
Ala Asn Gly Lys Val Ala Val Ile Val Ser Asn Asp His Ala Gly Lys
145 150 155 160
Leu Cys Gly Gly Xaa Trp Lys
165

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..705

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAG GAC TGC GTG TGC ACG GAC AAG GTG GAC AAC AAC ACC CTG CTC AAC	48
Gln Asp Cys Val Cys Thr Asp Lys Val Asp Asn Asn Thr Leu Leu Asn	
1 5 10 15	
GTC ATC GCC TGC ACC CAC GTG CCC TGC AAC ACC TCC TGC AGC CCT GGG	96
Val Ile Ala Cys Thr His Val Pro Cys Asn Thr Ser Cys Ser Pro Gly	
20 25 30	
TTC GAA CTC ATG GAG GCC CCC GGG GAG TGC TGT AAG AAG TGT GAA CAG	144
Phe Glu Leu Met Glu Ala Pro Gly Glu Cys Cys Lys Lys Cys Glu Gln	
35 40 45	
ACG CAC TGT ATC ATC AAA CGG CCC GAC AAC CAG CAC GTC ATC CTG AAG	192
Thr His Cys Ile Ile Lys Arg Pro Asp Asn Gln His Val Ile Leu Lys	
50 55 60	
CCC GGG GAC TTC AAG AGC GAC CCG AAG AAC AAC TGC ACA TTC TTC AGC	240
Pro Gly Asp Phe Lys Ser Asp Pro Lys Asn Asn Cys Thr Phe Phe Ser	
65 70 75 80	
TGC GTG AAG ATC CAC AAC CAG CTC ATC TCG TCC GTT TCC AAC ATC ACC	288
Cys Val Lys Ile His Asn Gln Leu Ile Ser Ser Val Ser Asn Ile Thr	
85 90 95	
TGC CCC AAC TTT GAT GCC AGC ATT TGC ATC CCG GGC TCC ATC ACA TTC	336
Cys Pro Asn Phe Asp Ala Ser Ile Cys Ile Pro Gly Ser Ile Thr Phe	
100 105 110	
ATG CCC AAT GGA TGC TGC AAG ACC TGC ACC CCT CGC AAT GAG ACC AGG	384
Met Pro Asn Gly Cys Cys Lys Thr Cys Thr Pro Arg Asn Glu Thr Arg	
115 120 125	
GTG CCC TGC TCC ACC GTC CCC GTC ACC ACG GAG GTT TCG TAC GCC GGC	432
Val Pro Cys Ser Thr Val Pro Val Thr Thr Glu Val Ser Tyr Ala Gly	
130 135 140	
TGC ACC AAG ACC GTC CTC ATG AAT CAT TGC TCC GGG TCC TGC GGG ACA	480
Cys Thr Lys Thr Val Leu Met Asn His Cys Ser Gly Ser Cys Gly Thr	
145 150 155 160	
TTT GTC ATG TAC TCG GCC AAG GCC CAG GCC CTG GAC CAC AGC TGC TCC	528
Phe Val Met Tyr Ser Ala Lys Ala Gln Ala Leu Asp His Ser Cys Ser	
165 170 175	
TGC TGC AAA GAG GAG AAA ACC AGC CAG CGT GAG GTG GTC CTG AGC TGC	576
Cys Cys Lys Glu Glu Lys Thr Ser Gln Arg Glu Val Val Leu Ser Cys	
180 185 190	
CCC AAT GGC GGC TCG CTG ACA CAC ACC TAC ACC CAC ATC GAG AGC TGC	624
Pro Asn Gly Gly Ser Leu Thr His Thr Tyr Thr His Ile Glu Ser Cys	
195 200 205	

CAG TGC CAG GAC ACC GTC TGC GGG CTC CCC ACC GGC ACC TCC CGC CGG	672
Gln Cys Gln Asp Thr Val Cys Gly Leu Pro Thr Gly Thr Ser Arg Arg	
210 215 220	
GCC CGG CGT TCC CCT AGG CAT CTG GGG AGC GGG TGAGCGGGGT GGGCACAGCC	725
Ala Arg Arg Ser Pro Arg His Leu Gly Ser Gly	
225 230 235	
CCTTCACTGC CCTCGACAGC TTTACCTCCC CCGGACCCTC TGAGCCTCCT AAGCTCGGCT	785
TCCTCTCTTC AGATATTTAT TGTCTGAGTT TTTGTTCAGT CCTTGCTTTC CAATAATAAA	845
CTCAGGGGGA CATGCAAAAA AAAAAAAAAA	874

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Asp Cys Val Cys Thr Asp Lys Val Asp Asn Asn Thr Leu Leu Asn	
1 5 10 15	
Val Ile Ala Cys Thr His Val Pro Cys Asn Thr Ser Cys Ser Pro Gly	
20 25 30	
Phe Glu Leu Met Glu Ala Pro Gly Glu Cys Cys Lys Lys Cys Glu Gln	
35 40 45	
Thr His Cys Ile Ile Lys Arg Pro Asp Asn Gln His Val Ile Leu Lys	
50 55 60	
Pro Gly Asp Phe Lys Ser Asp Pro Lys Asn Asn Cys Thr Phe Phe Ser	
65 70 75 80	
Cys Val Lys Ile His Asn Gln Leu Ile Ser Ser Val Ser Asn Ile Thr	
85 90 95	
Cys Pro Asn Phe Asp Ala Ser Ile Cys Ile Pro Gly Ser Ile Thr Phe	
100 105 110	
Met Pro Asn Gly Cys Cys Lys Thr Cys Thr Pro Arg Asn Glu Thr Arg	
115 120 125	
Val Pro Cys Ser Thr Val Pro Val Thr Thr Glu Val Ser Tyr Ala Gly	
130 135 140	
Cys Thr Lys Thr Val Leu Met Asn His Cys Ser Gly Ser Cys Gly Thr	
145 150 155 160	
Phe Val Met Tyr Ser Ala Lys Ala Gln Ala Leu Asp His Ser Cys Ser	

165

170

175

Cys Cys Lys Glu Glu Lys Thr Ser Gln Arg Glu Val Val Leu Ser Cys
180 185 190

Pro Asn Gly Gly Ser Leu Thr His Thr Tyr Thr His Ile Glu Ser Cys
195 200 205

Gln Cys Gln Asp Thr Val Cys Gly Leu Pro Thr Gly Thr Ser Arg Arg
210 215 220

Ala Arg Arg Ser Pro Arg His Leu Gly Ser Gly
225 230 235

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTGGTGCTA CCTGGCTCTC CTGTCTCTGC AGCTCTACAG GTGAGGCCCA GCAGAGGGAG	60
TAGGGCTCGC CATGTTTCTG GTGAGCCAAT TTGGCTGATC TTGGGTGTCT GAACAGCTAT	120
TGGGTCCACC CCAGTCCCTT TCAGCTGCTG CTTAATGCCC TGCTCTCTCC CTGGCCCACC	180
TTATAGAGAG CCCAAAGAGC TCCTGTAAGA GGGAGAACTC TATCTGTGGT TTATAATCTT	240
GCACGAGGCA CCAGAAGTCT CCCTGGGTCT TGTGAATGAA CTACATTTAT CCCCTTTCCT	300
GCCCCAACCA CAAACTCTTT CCTTCAAAGA GGGCCTGCCT GGTTCCTCC ACCCAACTGC	360
ACCATGAGAT CGGTCCAAGA GTCCATTCCC CAGGTGGGAG CCAACTGTCA GGGAGGTCTT	420
TCCCACCAA CATCTTTCAG TTGCTGGGAG GTGACCATAG GGCTCTGCTT TTAAAGATAT	480
GGCTGCTTCA AAGGCCAGAG TCACAGGAAG GACTTCTTCC AGGGAGATTA GTGGTGATGG	540
AGAGGAGAGT TAAAATGACC TCATGTCCTT CTTGTCCACG GTTTTGTTGA GTTTTCACTC	600
TTCTAATGCA AGGGTCTCAC ACTGTGAACC ACTTAGGATG TGATCACTTT CAGGTGGCCA	660
GGAATGTTGA ATGTCTTTGG CTCAGTTCAT CTAAAAAAGA TATCTATTG AAAGTTCTCA	720
GAGTTGTACA TATGTTTCAC AGTACAGGAT CTGTACATAA AAGTTTCTTT CCTAAACCAT	780
TCACCAAGAG CCAATATCTA GGCATTTCTT CGGTAGCACA AATTTTCTNA TTGCTTAGAA	840
AATTGTCCTC CCTGTTCTTT CTGTCTGNAG ACTTAAGTGA GTTAGGTCTT TAAGGAAAGC	900

AACGCTCCTC TGAAATGCTT GTCTTTTTTC TGTTGCCGAA ATAGCTGGTC CTTTTTCGGG	960
AGTTAGATGT ATAGAGTGTT TGTATGTAAA CATTCTTGT AGGCATCACC ATGAACANAG	1020
ATATATTTTC TATTTANTTA NTATATGTGC ACTTCAAGAA GTCAGTGTCA GAGAAATAAA	1080
GAATTGTCTT AAATGTCATG ATTGGAGATG TCCTTTGCAT TGCTTGGAAG GGGTGTACCT	1140
AGAGCCAAGG AAATTGGCTC TGGTTTGGA AAATTTTGCT GTTATTATAG TAAACATACA	1200
AAGGATGTC	1209

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..405

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG AGT CCT GTG AAA AAC AAT GTG GGC AGA GGC CTA AAC ATC GCC CTG	48
Met Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu	
1 5 10 15	
GTG AAT GGA ACC ACG GGA GCT GTG CTG GGA CAG AAG GCA TTT GAC ATG	96
Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp Met	
20 25 30	
TAC TCT GGA GAT GTT ATG CAC CTA GTG AAA TTC CTT AAA GAA ATT CCG	144
Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu Ile Pro	
35 40 45	
GGG GGT GCA CTG GTG CTG GTG GCC TCC TAC GAC GAT CCA GGG ACC AAA	192
Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro Gly Thr Lys	
50 55 60	
ATG AAC GAT GAA AGC AGG AAA CTC TTC TCT GAC TTG GGG AGT TCC TAC	240
Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu Gly Ser Ser Tyr	
65 70 75 80	
GCA AAA CAA CTG GGC TTC CGG GAC AGC TGG GTC TTC ATA GGA GCC AAA	288
Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val Phe Ile Gly Ala Lys	

85	90	95	
GAC CTC AGG GGT AAA AGC CCC TTT GAG CAG TTC TTA AAG AAC AGC CCA			336
Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln Phe Leu Lys Asn Ser Pro			
100	105	110	
GAC ACA AAC AAA TAC GAG GGA TGG CCA GAG CTG CTG GAG ATG GAG GGC			384
Asp Thr Asn Lys Tyr Glu Gly Trp Pro Glu Leu Leu Glu Met Glu Gly			
115	120	125	
TGC ATG CCC CCG AAG CCA TTT TAGGGTGGCT GTGGCTCTTC CTCAGCCAGG			435
Cys Met Pro Pro Lys Pro Phe			
130	135		
GGCCTGAAGA AGYTCCTGCC TGCATTAGGA GTCANAGCCC GGCAGGCTGN AGGAGGAGGA			495
GCAGGGGGTG CTGCGTGGAA GGTGCTGCAG GCCTTGCACG CTGTGTCGCG CCT			548

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu				
1	5	10	15	
Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp Met				
20	25	30		
Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu Ile Pro				
35	40	45		
Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro Gly Thr Lys				
50	55	60		
Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu Gly Ser Ser Tyr				
65	70	75	80	
Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val Phe Ile Gly Ala Lys				
85	90	95		
Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln Phe Leu Lys Asn Ser Pro				
100	105	110		
Asp Thr Asn Lys Tyr Glu Gly Trp Pro Glu Leu Leu Glu Met Glu Gly				
115	120	125		
Cys Met Pro Pro Lys Pro Phe				
130	135			

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 878 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

T GTC TAC TCA AGG TAT TTC ACA ACT TAT GAC ACG AAT GGT AGA TAC	46
Val Tyr Ser Arg Tyr Phe Thr Thr Tyr Asp Thr Asn Gly Arg Tyr	
1 5 10 15	
AGT GTA AAA GTG CGG GCT CTG GGA GGA GTT AAC GCA GCC AGA CGG AGA	94
Ser Val Lys Val Arg Ala Leu Gly Gly Val Asn Ala Ala Arg Arg Arg	
20 25 30	
GTG ATA CCC CAG CAG AGT GGA GCA CTG TAC ATA CCT GGC TGG ATT GAG	142
Val Ile Pro Gln Gln Ser Gly Ala Leu Tyr Ile Pro Gly Trp Ile Glu	
35 40 45	
AAT GAT GAA ATA CAA TGG AAT CCA CCA AGA CCT GAA ATT AAT AAG GAT	190
Asn Asp Glu Ile Gln Trp Asn Pro Pro Arg Pro Glu Ile Asn Lys Asp	
50 55 60	
GAT GTT CAA CAC AAG CAA GTG TGT TTC AGC AGA ACA TCC TCG GGA GGC	238
Asp Val Gln His Lys Gln Val Cys Phe Ser Arg Thr Ser Ser Gly Gly	
65 70 75	
TCA TTT GTG GCT TCT GAT GTC CCA AAT GCT CCC ATA CCT GAT CTC TTC	286
Ser Phe Val Ala Ser Asp Val Pro Asn Ala Pro Ile Pro Asp Leu Phe	
80 85 90 95	
CCA CCT GGC CAA ATC ACC GAC CTG AAG GCG GAA ATT CAC GGG GGC AGT	334
Pro Pro Gly Gln Ile Thr Asp Leu Lys Ala Glu Ile His Gly Gly Ser	
100 105 110	
CTC ATT AAT CTG ACT TGG ACA GCT CCT GGG GAT GAT TAT GAC CAT GGA	382
Leu Ile Asn Leu Thr Trp Thr Ala Pro Gly Asp Asp Tyr Asp His Gly	
115 120 125	
ACA GCT CAC AAG TAT ATC ATT CGA ATA AGT ACA AGT ATT CTT GAT CTC	430
Thr Ala His Lys Tyr Ile Ile Arg Ile Ser Thr Ser Ile Leu Asp Leu	
130 135 140	
AGA GAC AAG TTC AAT GAA TCT CTT CAA GTG AAT ACT ACT GCT CTC ATC	478
Arg Asp Lys Phe Asn Glu Ser Leu Gln Val Asn Thr Thr Ala Leu Ile	
145 150 155	

CCA AAG GAA GCC AAC TCT GAG GAA GTC TTT TTG TTT AAA CCA GAA AAC	526
Pro Lys Glu Ala Asn Ser Glu Glu Val Phe Leu Phe Lys Pro Glu Asn	
160 165 170 175	
ATT ACT TTT GAA AAT GGC ACA GAT CTT TTC ATT GCT ATT CAG GCT GTT	574
Ile Thr Phe Glu Asn Gly Thr Asp Leu Phe Ile Ala Ile Gln Ala Val	
180 185 190	
GAT AAG GTC GAT CTG AAA TCA GAA ATA TCC AAC ATT GCA CGA GTA TCT	622
Asp Lys Val Asp Leu Lys Ser Glu Ile Ser Asn Ile Ala Arg Val Ser	
195 200 205	
TTG TTT ATT CCT CCA CAG ACT CCG CCA GAG ACA CCT AGT CCT GAT GAA	670
Leu Phe Ile Pro Pro Gln Thr Pro Pro Glu Thr Pro Ser Pro Asp Glu	
210 215 220	
ACG TCT GCT CCT TGT GCCTAATATT CATATCAACA GCACCATTCC TGGCATTAC	725
Thr Ser Ala Pro Cys	
225	
ATTTTAAAAA TTATGTGGAA GTGGGTAGGA GAACTGCAGT TGTCATAGN CTAGGGGTGA	785
ATTTTTGTGC GGTGAATAAA TAATSATTTC ANCCTTTTTT TGRTTTATAA AAAAACGGNT	845
NCCCATTGGG NNTNTNGNGG GGGGGNNTTT TAA	878

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Tyr Ser Arg Tyr Phe Thr Thr Tyr Asp Thr Asn Gly Arg Tyr Ser	
1 5 10 15	
Val Lys Val Arg Ala Leu Gly Gly Val Asn Ala Ala Arg Arg Arg Val	
20 25 30	
Ile Pro Gln Gln Ser Gly Ala Leu Tyr Ile Pro Gly Trp Ile Glu Asn	
35 40 45	
Asp Glu Ile Gln Trp Asn Pro Pro Arg Pro Glu Ile Asn Lys Asp Asp	
50 55 60	
Val Gln His Lys Gln Val Cys Phe Ser Arg Thr Ser Ser Gly Gly Ser	
65 70 75 80	
Phe Val Ala Ser Asp Val Pro Asn Ala Pro Ile Pro Asp Leu Phe Pro	
85 90 95	

Pro Gly Gln Ile Thr Asp Leu Lys Ala Glu Ile His Gly Gly Ser Leu
 100 105 110
 Ile Asn Leu Thr Trp Thr Ala Pro Gly Asp Asp Tyr Asp His Gly Thr
 115 120 125
 Ala His Lys Tyr Ile Ile Arg Ile Ser Thr Ser Ile Leu Asp Leu Arg
 130 135 140
 Asp Lys Phe Asn Glu Ser Leu Gln Val Asn Thr Thr Ala Leu Ile Pro
 145 150 155 160
 Lys Glu Ala Asn Ser Glu Glu Val Phe Leu Phe Lys Pro Glu Asn Ile
 165 170 175
 Thr Phe Glu Asn Gly Thr Asp Leu Phe Ile Ala Ile Gln Ala Val Asp
 180 185 190
 Lys Val Asp Leu Lys Ser Glu Ile Ser Asn Ile Ala Arg Val Ser Leu
 195 200 205
 Phe Ile Pro Pro Gln Thr Pro Pro Glu Thr Pro Ser Pro Asp Glu Thr
 210 215 220
 Ser Ala Pro Cys
 225

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..490

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 2..490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

A GTC GCT CTC CTA GCC CTT CTC TGT GCC TCA CCC TCT GGC AAT GCC	46
Val Ala Leu Leu Ala Leu Leu Cys Ala Ser Pro Ser Gly Asn Ala	
1 5 10 15	
ATT CAG GCC AGG TCT TCC TCC TAT AGT GGA GAG TAT GGA GGT GGT GGT	94
Ile Gln Ala Arg Ser Ser Ser Tyr Ser Gly Glu Tyr Gly Gly Gly Gly	
20 25 30	

GGA AAG CGA TTC TCT CAT TCT GGC AAC CAG TTG GAC GGC CCC ATC ACC	142
Gly Lys Arg Phe Ser His Ser Gly Asn Gln Leu Asp Gly Pro Ile Thr	
35 40 45	
GCC CTC CGG GTC CGA GTC AAC ACA TAC TAC ATC GTA GGT CTT CAG GTG	190
Ala Leu Arg Val Arg Val Asn Thr Tyr Tyr Ile Val Gly Leu Gln Val	
50 55 60	
CGC TAT GGC AAG GTG TGG AGC GAC TAT GTG GGT GGT CGC AAC GGA GAC	238
Arg Tyr Gly Lys Val Trp Ser Asp Tyr Val Gly Gly Arg Asn Gly Asp	
65 70 75	
CTG GAG GAG ATC TTT CTG CAC CCT GGG GAA TCA GTG ATC CAG GTT TCT	286
Leu Glu Glu Ile Phe Leu His Pro Gly Glu Ser Val Ile Gln Val Ser	
80 85 90 95	
GGG AAG TAC AAG TGG TAC CTG AAG AAG CTG GTA TTT GTG ACA GAC AAG	334
Gly Lys Tyr Lys Trp Tyr Leu Lys Lys Leu Val Phe Val Thr Asp Lys	
100 105 110	
GGC CGC TAT CTG TCT TTT GGG AAA GAC AGT GGC ACA AGT TTC AAT GCC	382
Gly Arg Tyr Leu Ser Phe Gly Lys Asp Ser Gly Thr Ser Phe Asn Ala	
115 120 125	
GTC CCC TTG CAC CCC AAC ACC GTG CTC CGC TTC ATC AGT GGC CGG TCT	430
Val Pro Leu His Pro Asn Thr Val Leu Arg Phe Ile Ser Gly Arg Ser	
130 135 140	
GGT TCT CTC ATC GAT GCC ATT GGC CTG CAC TGG GAT GTT TAC CCC ACT	478
Gly Ser Leu Ile Asp Ala Ile Gly Leu His Trp Asp Val Tyr Pro Thr	
145 150 155	
AGC TGC AGC AGA TGCTGAGCCT CCTCTCCTTG GCAGGGGCAC TGTGATGAGG	530
Ser Cys Ser Arg	
160	
AGTAAGAACT CCTTATCACT AACCCCCATC	560

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Val Ala Leu Leu Ala Leu Leu Cys Ala Ser Pro Ser Gly Asn Ala Ile	
1 5 10 15	
Gln Ala Arg Ser Ser Ser Tyr Ser Gly Glu Tyr Gly Gly Gly Gly Gly	
20 25 30	
Lys Arg Phe Ser His Ser Gly Asn Gln Leu Asp Gly Pro Ile Thr Ala	
35 40 45	

Leu Arg Val Arg Val Asn Thr Tyr Tyr Ile Val Gly Leu Gln Val Arg
 50 55 60
 Tyr Gly Lys Val Trp Ser Asp Tyr Val Gly Gly Arg Asn Gly Asp Leu
 65 70 75 80
 Glu Glu Ile Phe Leu His Pro Gly Glu Ser Val Ile Gln Val Ser Gly
 85 90 95
 Lys Tyr Lys Trp Tyr Leu Lys Lys Leu Val Phe Val Thr Asp Lys Gly
 100 105 110
 Arg Tyr Leu Ser Phe Gly Lys Asp Ser Gly Thr Ser Phe Asn Ala Val
 115 120 125
 Pro Leu His Pro Asn Thr Val Leu Arg Phe Ile Ser Gly Arg Ser Gly
 130 135 140
 Ser Leu Ile Asp Ala Ile Gly Leu His Trp Asp Val Tyr Pro Thr Ser
 145 150 155 160
 Cys Ser Arg

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAACTTGCT GTTTTGTTCC TGTGTCTTGT CTTTGGTTGG TATTTTCAGTA AGTTTTTGGT	60
ATTCTCAAAT TTTATCTAAA TGGATAAACT ATTAACATAG AACATAAACC CCAATTCTCC	120
ATTTTCATTTT TCTCTTAGGC ATGAATCATA CAAAACCTCAA TATAGAGCAA TGTTTGTAAT	180
GAATTGTTCT ATTAACAAAG AGGAGGTTCT AAGATATAAA GCCTCAGAGA ACAGGAAGAA	240
AAGGCGGGTC CATAAGAAGA TGAGGTCTAA CCGGGAAGAT GCTGCTGAGA AGGCAGAGAC	300
AGATGTGGAA GAAATCTATC ACCCAGTCAT GTGCACTGAA TGTTCCACTG AAGTGGCAGT	360
TTACGACAAG GATGAAGTCT TTCATTTTTT CAATGTTTTA GCAAGCCATT CCTAACAGC	420
CCAAGTGGCA TTTAATTACC CAATACTGTA TATAAGGCAA ATATGGACAG TTAAGTTTCT	480
CTTGCCTGTT CATATCCTTC AGTGACATTG AGGAAGCAGT GTTTCTCTTT TTAAAGGGGA	540

ATAGTTGTCA ACCTTCATTC ATCTCTTACA TCTTTCACCC TCTCCTTTTT TTTTCTTTG	600
ATTTTCCCCC TTATTGATGG GACTGATATT CATTCTGTTT TTGATGAACA TTTGGAAACT	660
GTCGGGCTTT TTATTAAAGC TCTGTAGAAT TAAAATGTTC TGGAATTAT	709

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 125..367

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 125..367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAGGAGGGAG AGCCTTCCCC AAGCAAACAA TCCAGAGCAG CTGTGCAAAC AACGGTGCAT	60
AAATAAGGCC TCCTGGACCA TGAATGCGAG TCCGCTGAGC TCGTACCGG AGCCCACGGT	120
GGTC ATG GCT GCC AGA GCG CTC TGC ATG CTG GGG CTG GTC CTG GCC TTG	169
Met Ala Ala Arg Ala Leu Cys Met Leu Gly Leu Val Leu Ala Leu	
1 5 10 15	
CTG TCC TCC AGC TCT GCT GAG GAG TAC GTG GGC CTG TCT GCA AAC CAG	217
Leu Ser Ser Ser Ser Ala Glu Glu Tyr Val Gly Leu Ser Ala Asn Gln	
20 25 30	
TGT GCC GTG CCA GCC AAG GAC AGG GTG GAC TGC GGC TAC CCC CAT GTC	265
Cys Ala Val Pro Ala Lys Asp Arg Val Asp Cys Gly Tyr Pro His Val	
35 40 45	
ACC CCC AAG GAG TGC AAC AAC CGG GGC TGC TGC TTT GAC TCC AGG ATC	313
Thr Pro Lys Glu Cys Asn Asn Arg Gly Cys Cys Phe Asp Ser Arg Ile	
50 55 60	
CCT GGA GTG CCT TGG TGT TTC AAG CCC CTG ACA GGG AAG CAG GAA TGC	361
Pro Gly Val Pro Trp Cys Phe Lys Pro Leu Thr Gly Lys Gln Glu Cys	
65 70 75	
ACC TTC TGAGGCACCT CCAGCTGCCC CCCGGCCGGG GGATGCGAGG CTCGGAGCAC	417
Thr Phe	
80	
CCTTGCCCCG CTGTGATTGC TGCCAGGCAC TGTTTCATCTC AGCTTTTCTG TCCCTTTGCT	477

CCCGGAAGCG CTTCTGCTGA AAGTTCATAT CTGGAGCCTG ATGTTTAACG TAGTCCCATG 537
 CTCCACCCGA AAAAAAAAAA AAAAAAAAAA AAA 570

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ala Ala Arg Ala Leu Cys Met Leu Gly Leu Val Leu Ala Leu Leu
 1 5 10 15
 Ser Ser Ser Ser Ala Glu Glu Tyr Val Gly Leu Ser Ala Asn Gln Cys
 20 25 30
 Ala Val Pro Ala Lys Asp Arg Val Asp Cys Gly Tyr Pro His Val Thr
 35 40 45
 Pro Lys Glu Cys Asn Asn Arg Gly Cys Cys Phe Asp Ser Arg Ile Pro
 50 55 60
 Gly Val Pro Trp Cys Phe Lys Pro Leu Thr Gly Lys Gln Glu Cys Thr
 65 70 75 80
 Phe

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 42..1010

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 42..1010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAGCTCTTCT CACAGGACCA GCCACTAGCG CAGCTCGAGC G ATG GCC TAT GTC 53
 Met Ala Tyr Val
 1

CCC GCA CCG GGC TAC CAG CCC ACC TAC AAC CCG ACG CTG CCT TAC TAC	101
Pro Ala Pro Gly Tyr Gln Pro Thr Tyr Asn Pro Thr Leu Pro Tyr Tyr	
5 10 15 20	
CAG CCC ATC CCG GGC GGG CTC AAC GTG GGA ATG TCT GTT TAC ATC CAA	149
Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser Val Tyr Ile Gln	
25 30 35	
GGA GTG GCC AGC GAG CAC ATG AAG CGG TTC TTC GTG AAC TTT GTG GTT	197
Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val Asn Phe Val Val	
40 45 50	
GGG CAG GAT CCG GGC TCA GAC GTC GCC TTC CAC TTC AAT CCG CGG TTT	245
Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe Asn Pro Arg Phe	
55 60 65	
GAC GGC TGG GAC AAG GTG GTC TTC AAC ACG TTG CAG GGC GGG AAG TGG	293
Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln Gly Gly Lys Trp	
70 75 80	
GGC AGC GAG GAG AGG AAG AGG AGC ATG CCC TTC AAA AAG GGT GCC GCC	341
Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys Lys Gly Ala Ala	
85 90 95 100	
TTT GAG CTG GTC TTC ATA GTC CTG GCT GAG CAC TAC AAG GTG GTG GTA	389
Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr Lys Val Val Val	
105 110 115	
AAT GGA AAT CCC TTC TAT GAG TAC GGG CAC CGG CTT CCC CTA CAG ATG	437
Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu Pro Leu Gln Met	
120 125 130	
GTC ACC CAC CTG CAA GTG GAT GGG GAT CTG CAA CTT CAA TCA ATC AAC	485
Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu Gln Ser Ile Asn	
135 140 145	
TTC ATC GGA GGC CAG CCC CTC CGG CCC CAG GGA CCC CCG ATG ATG CCA	533
Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro Pro Met Met Pro	
150 155 160	
CCT TAC CCT GGT CCC GGA CAT TGC CAT CAA CAG CTG AAC AGC CTG CCC	581
Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu Asn Ser Leu Pro	
165 170 175 180	
ACC ATG GAA GGA CCC CCA ACC TTC AAC CCG CCT GTG CCA TAT TTC GGG	629
Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val Pro Tyr Phe Gly	
185 190 195	
AGG CTG CAA GGA GGG CTC ACA GCT CGA AGA ACC ATC ATC ATC AAG GGC	677
Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile Ile Ile Lys Gly	
200 205 210	
TAT GTG CCT CCC ACA GGC AAG AGC TTT GCT ATC AAC TTC AAG GTG GGC	725
Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn Phe Lys Val Gly	
215 220 225	

TCC TCA GGG GAC ATA GCT CTG CAC ATT AAT CCC CGC ATG GGC AAC GGT Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg Met Gly Asn Gly 230 235 240	773
ACC GTG GTC CGG AAC AGC CTT CTG AAT GGC TCG TGG GGA TCC GAG GAG Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp Gly Ser Glu Glu 245 250 255 260	821
AAG AAG ATC ACC CAC AAC CCA TTT GGT CCC GGA CAG TTC TTT GAT CTG Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln Phe Phe Asp Leu 265 270 275	869
TCC ATT CGC TGT GGC TTG GAT CGC TTC AAG GTT TAC GCC AAT GGC CAG Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr Ala Asn Gly Gln 280 285 290	917
CAC CTC TTT GAC TTT GCC CAT CGC CTC TCG GCC TTC CAG AGG GTG GAC His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe Gln Arg Val Asp 295 300 305	965
ACA TTG GAA ATC CAG GGT GAT GTC ACC TTG TCC TAT GTC CAG ATC Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr Val Gln Ile 310 315 320	1010
TAATCTATTC CTGGGGCCAT AACTCATGGG AAAACAGAAT TATCCCCTAG GACTCCTTTC	1070
TAAGCCCCTA ATAAAATGTC TGAGGGTGTC TCAAAAAAAAA AAAAAAAAAA A	1121

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ala Tyr Val Pro Ala Pro Gly Tyr Gln Pro Thr Tyr Asn Pro Thr 1 5 10 15
Leu Pro Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser 20 25 30
Val Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val 35 40 45
Asn Phe Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe 50 55 60
Asn Pro Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln 65 70 75 80
Gly Gly Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys 85 90 95

Lys Gly Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr
 100 105 110
 Lys Val Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu
 115 120 125
 Pro Leu Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu
 130 135 140
 Gln Ser Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro
 145 150 155 160
 Pro Met Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu
 165 170 175
 Asn Ser Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val
 180 185 190
 Pro Tyr Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile
 195 200 205
 Ile Ile Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn
 210 215 220
 Phe Lys Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg
 225 230 235 240
 Met Gly Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp
 245 250 255
 Gly Ser Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln
 260 265 270
 Phe Phe Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr
 275 280 285
 Ala Asn Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe
 290 295 300
 Gln Arg Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr
 305 310 315 320
 Val Gln Ile

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..603

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTT GAT ATT AAA ACC AGT GAA ACC AAA CAT GAC ACC TCT CTG AAA CCT	48
Val Asp Ile Lys Thr Ser Glu Thr Lys His Asp Thr Ser Leu Lys Pro	
1 5 10 15	
ATT AGT GTC TCC TAC AAC CCA GCC ACA GCC AAA GAA ATT ATC AAT GTG	96
Ile Ser Val Ser Tyr Asn Pro Ala Thr Ala Lys Glu Ile Ile Asn Val	
20 25 30	
GGG CAT TCC TTC CAT GTA AAT TTT GAG GAC AAC GAT AAC CGA TCA GTG	144
Gly His Ser Phe His Val Asn Phe Glu Asp Asn Asp Asn Arg Ser Val	
35 40 45	
CTG AAA GGT GGT CCT TTC TCT GAC AGC TAC AGG CTC TTT CAG TTC CAT	192
Leu Lys Gly Gly Pro Phe Ser Asp Ser Tyr Arg Leu Phe Gln Phe His	
50 55 60	
TTT CAC TGG GGC AGT ACA AAT GAG CAT GGT TCA GAA CAT ACA GTG GAT	240
Phe His Trp Gly Ser Thr Asn Glu His Gly Ser Glu His Thr Val Asp	
65 70 75 80	
GGA GTC AAA TAT TCT GCC GAG CTT CAC GTG GCT CAC TGG AAT TCT GCA	288
Gly Val Lys Tyr Ser Ala Glu Leu His Val Ala His Trp Asn Ser Ala	
85 90 95	
AAG TAC TCC AGC CTT GCT GAA GCT GCC TCA AAG GCT GAT GGT TTG GCA	336
Lys Tyr Ser Ser Leu Ala Glu Ala Ala Ser Lys Ala Asp Gly Leu Ala	
100 105 110	
GTT ATT GGT GTT TTG ATG AAG GTT GGT GAG GCC AAC CCA AAG CTG CAG	384
Val Ile Gly Val Leu Met Lys Val Gly Glu Ala Asn Pro Lys Leu Gln	
115 120 125	
AAA GTA CTT GAT GCC CTC CAA GCA ATT AAA ACC AAG GGC AAA CGA GCC	432
Lys Val Leu Asp Ala Leu Gln Ala Ile Lys Thr Lys Gly Lys Arg Ala	
130 135 140	
CCA TTC ACA AAT TTT GAC CCC TCT ACT CTC CTT CCT TCA TCC CTG GAT	480
Pro Phe Thr Asn Phe Asp Pro Ser Thr Leu Leu Pro Ser Ser Leu Asp	
145 150 155 160	
TTC TGG ACC TAC CCT GGC TCT CTG ACT CAT CCT CCT CTT TAT GAG AGT	528
Phe Trp Thr Tyr Pro Gly Ser Leu Thr His Pro Pro Leu Tyr Glu Ser	
165 170 175	
GTA ACT TGG ATC ATC TGT AAG GAG AGC ATC AGT GTC AGT TCA GAG CAG	576
Val Thr Trp Ile Ile Cys Lys Glu Ser Ile Ser Val Ser Ser Glu Gln	
180 185 190	

TTG GCA CAA TTC CGG AGC CTT CTA TCA AT
 Leu Ala Gln Phe Arg Ser Leu Leu Ser
 195 200

605

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Val	Asp	Ile	Lys	Thr	Ser	Glu	Thr	Lys	His	Asp	Thr	Ser	Leu	Lys	Pro	1	5	10	15
Ile	Ser	Val	Ser	Tyr	Asn	Pro	Ala	Thr	Ala	Lys	Glu	Ile	Ile	Asn	Val	20	25	30	
Gly	His	Ser	Phe	His	Val	Asn	Phe	Glu	Asp	Asn	Asp	Asn	Arg	Ser	Val	35	40	45	
Leu	Lys	Gly	Gly	Pro	Phe	Ser	Asp	Ser	Tyr	Arg	Leu	Phe	Gln	Phe	His	50	55	60	
Phe	His	Trp	Gly	Ser	Thr	Asn	Glu	His	Gly	Ser	Glu	His	Thr	Val	Asp	65	70	75	80
Gly	Val	Lys	Tyr	Ser	Ala	Glu	Leu	His	Val	Ala	His	Trp	Asn	Ser	Ala	85	90	95	
Lys	Tyr	Ser	Ser	Leu	Ala	Glu	Ala	Ala	Ser	Lys	Ala	Asp	Gly	Leu	Ala	100	105	110	
Val	Ile	Gly	Val	Leu	Met	Lys	Val	Gly	Glu	Ala	Asn	Pro	Lys	Leu	Gln	115	120	125	
Lys	Val	Leu	Asp	Ala	Leu	Gln	Ala	Ile	Lys	Thr	Lys	Gly	Lys	Arg	Ala	130	135	140	
Pro	Phe	Thr	Asn	Phe	Asp	Pro	Ser	Thr	Leu	Leu	Pro	Ser	Ser	Leu	Asp	145	150	155	160
Phe	Trp	Thr	Tyr	Pro	Gly	Ser	Leu	Thr	His	Pro	Pro	Leu	Tyr	Glu	Ser	165	170	175	
Val	Thr	Trp	Ile	Ile	Cys	Lys	Glu	Ser	Ile	Ser	Val	Ser	Ser	Glu	Gln	180	185	190	
Leu	Ala	Gln	Phe	Arg	Ser	Leu	Leu	Ser	195	200									

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 559 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 2..469

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 2..469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

C GGC TCC GGG CGG GCG TGG CCA GTG ACT AGA AGG CGA GGC GCC GCG	46
Gly Ser Gly Arg Ala Trp Pro Val Thr Arg Arg Arg Gly Ala Ala	
1 5 10 15	
GGA CCA TGG CGG CGG CGG CGG ACG AGC GGA GTC CAG AGG CGA GAA GAC	94
Gly Pro Trp Arg Arg Arg Arg Thr Ser Gly Val Gln Arg Arg Glu Asp	
20 25 30	
GAG GAA GAG GAG GAG CAG TTG GTT CTG GTG GAA TTA TCA GGA ATT ATT	142
Glu Glu Glu Glu Glu Gln Leu Val Leu Val Glu Leu Ser Gly Ile Ile	
35 40 45	
GAT TCA GAC TTC CTC TCA AAA TGT GAA AAT AAA TGC AAG GTT TTG GGC	190
Asp Ser Asp Phe Leu Ser Lys Cys Glu Asn Lys Cys Lys Val Leu Gly	
50 55 60	
ATT GAC ACT GAG AGG CCC ATT CTG GCA ATG GAC AGC TGT GTC TTT GCT	238
Ile Asp Thr Glu Arg Pro Ile Leu Ala Met Asp Ser Cys Val Phe Ala	
65 70 75	
GGG GAG TAT GAA GAC ACT CTA GGG ACC TGT GTT ATA TTT GAA GAA AAT	286
Gly Glu Tyr Glu Asp Thr Leu Gly Thr Cys Val Ile Phe Glu Glu Asn	
80 85 90 95	
GTT GAA CAT GCT GAT ACA GAA GGC AAT AAT AAA ACA GTG CTA AAA TAT	334
Val Glu His Ala Asp Thr Glu Gly Asn Asn Lys Thr Val Leu Lys Tyr	
100 105 110	
AAA TGC CAT ACA ATG AAG AAG CTC AGC ATG ACA AGA ACT CTC CTG ACA	382
Lys Cys His Thr Met Lys Lys Leu Ser Met Thr Arg Thr Leu Leu Thr	
115 120 125	
GAG AAG AAG GAA GGA GAA GAA AAC ATA GGT GGG GTG GAA TGG CTG CAA	430
Glu Lys Lys Glu Gly Glu Glu Asn Ile Gly Gly Val Glu Trp Leu Gln	
130 135 140	
ATA AGG ATA TGG TTT CTC CCT TTG ACC CAA CAG GTT TGT TAACTTTTCT	479
Ile Arg Ile Trp Phe Leu Pro Leu Thr Gln Gln Val Cys	

145

150

155

ACCATGAAAT TGAGGACGAG GAAGTGGTAG CTTTCAGCCC CGTTAAATCT TTGGATTGG 539
 GAGGGGGTGG GGTTCATG 559

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Ser Gly Arg Ala Trp Pro Val Thr Arg Arg Arg Gly Ala Ala Gly
 1 5 10 15
 Pro Trp Arg Arg Arg Arg Thr Ser Gly Val Gln Arg Arg Glu Asp Glu
 20 25 30
 Glu Glu Glu Glu Gln Leu Val Leu Val Glu Leu Ser Gly Ile Ile Asp
 35 40 45
 Ser Asp Phe Leu Ser Lys Cys Glu Asn Lys Cys Lys Val Leu Gly Ile
 50 55 60
 Asp Thr Glu Arg Pro Ile Leu Ala Met Asp Ser Cys Val Phe Ala Gly
 65 70 75 80
 Glu Tyr Glu Asp Thr Leu Gly Thr Cys Val Ile Phe Glu Glu Asn Val
 85 90 95
 Glu His Ala Asp Thr Glu Gly Asn Asn Lys Thr Val Leu Lys Tyr Lys
 100 105 110
 Cys His Thr Met Lys Lys Leu Ser Met Thr Arg Thr Leu Leu Thr Glu
 115 120 125
 Lys Lys Glu Gly Glu Glu Asn Ile Gly Gly Val Glu Trp Leu Gln Ile
 130 135 140
 Arg Ile Trp Phe Leu Pro Leu Thr Gln Gln Val Cys
 145 150 155

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGGCAGAAG AAAGATAGGT TGGAGACAAT TGATTGCTCG ATGATATAAA ATGTTAAGTA	60
CCATGAATGN ATGCTGTTAG GCTGGAATGC GCCAAGATAA AAGGTGGGGC ATGGCATCAA	120
AAGGTAGGTC AACATATTAA ATAATTCCAT GTATTGAAAT ATCCAGAAAA TATATAGACA	180
GATCTATAGA GATAGAAACT GGTCTGCCCA GGACTAGGGG TTGTCTAAGG ATAAGGAGCT	240
TCTTTTTTGG ATGGTGAAAT AACCTAAAAT ATATTGTGCC ATTGTTTGCA CAACTTTGTG	300
GAATATATTA AAAACCGGTT AATTGTACTC ACTAAAATGT CTCCTTCTT AAATTTAAGC	360
TGTTTNCTGG ACAAGAAAAA GGGAAAGNNA CCAAGGGGNA AAAAATTTT	409

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCCTGGGCT TTGGGGGGGT CCCAAACATG GTATGCAGAA ATGTGATGGT TACAGGTCAG	60
TACAACCTCA GTCCTTAGAA CCCCTCCACA CTTCAGCTCT GCACCCACTT TCCTGTCATT	120
TATTTATATA GGACTGTAGT TTTTTTTAGT TCGAGAGCCT TTCGAAGCTT AATTTATATT	180
CTTCTTTTGT ACCTTTTTTC TAAAATTACC AAAGATATTA CACAAAGGTA AATTAATGTT	240
CTCTGTTTTA TGCTTTATCT GATGGAGGCA AATATCCTCT TATTGTTGAT CAAAGGGGGC	300
AAAAGAATTT AGAGGCAAAT GAACAAGCGA TAGGCTATTG CAACCTGAGA AAGAGAACTG	360
NTCCTTCCAT CGTAAATTTA GNAGNCCAAG TAGGTAATGG GAACCAAAGT TGTTACTTTT	420
TTCTAGTAGT TATTTTTCCT TTTTNNNTT TTGTGGTACC TCTTACAGNG NCCCAAACT	480
CCATTCTCTT TAAAGGGGTT TTTATGGGGG GCTTACTGCA GGTAAAAAAT TGGGGNCCAC	540
CATTTTAAAA GGGGGGCTAC CAGAAGGGAG GGGGGTCCCC NTTNCNAAAA AAAAAAATTG	600

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGCTTCCGG CTCGTATG

18

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGGTTTTCCC AGTCACGAC

19